TAXONOMY OF JUNIPERUS, SECTION JUNIPERUS: SEQUENCE ANALYSIS OF nrDNA AND FIVE cpDNA REGIONS

Robert P. Adams

Biology Department, Baylor University, Box 97388, Waco, TX 76798, USA email Robert Adams@baylor.edu

and

Andrea E. Schwarzbach Department of Biomedicine, University of Texas at Brownsville, Brownsville, TX 78520, USA.

ABSTRACT

A robust analysis of Juniperus, sect. Juniperus is presented based on nrDNA and five cpDNA regions. The section is clearly divided into two groups composed of blue and red seed cone species and is composed of four major clades: J. communis and allies; J. cedrus - oxvcedrus allies: J. brevifolia - deltoides - navicularis: and a loose clade of J. formosana, f. var. mairei, and J. communis var. jackii. Juniperus c. var. jackii was found to be the most divergent taxon in the blue seed cone group and is recognized at the specific level: Juniperus jackii (Rehder) R. P. Adams, comb. nov. Juniperus formosana and var. mairei were found to be very distinct and the DNA data supports the recognition of J. mairei Lemee & H. Lev. The DNA data also support the recognition of J. lutchuensis Koidz. and J. communis var. hemisphaerica (J. & C. Presl) Parl. The putative J. communis var. saxatilis from Kamchatka peninsula, Russia was found to be unique in its DNA sequence and was recognized as: Juniperus communis var. kamchatkensis R. P. Adams, var. nov. Phytologia 94(2): 280-297 (August 1, 2012).

KEY WORDS: Phylogeny, *Juniperus*, section *Juniperus*, nrDNA, petN-psbM, trnS-trnG, trnD-trnT, ycf3 intron 2, trnK-matK, *J. jackii*, *J. c.* var. *kamchatkensis*.